

FIG. 1

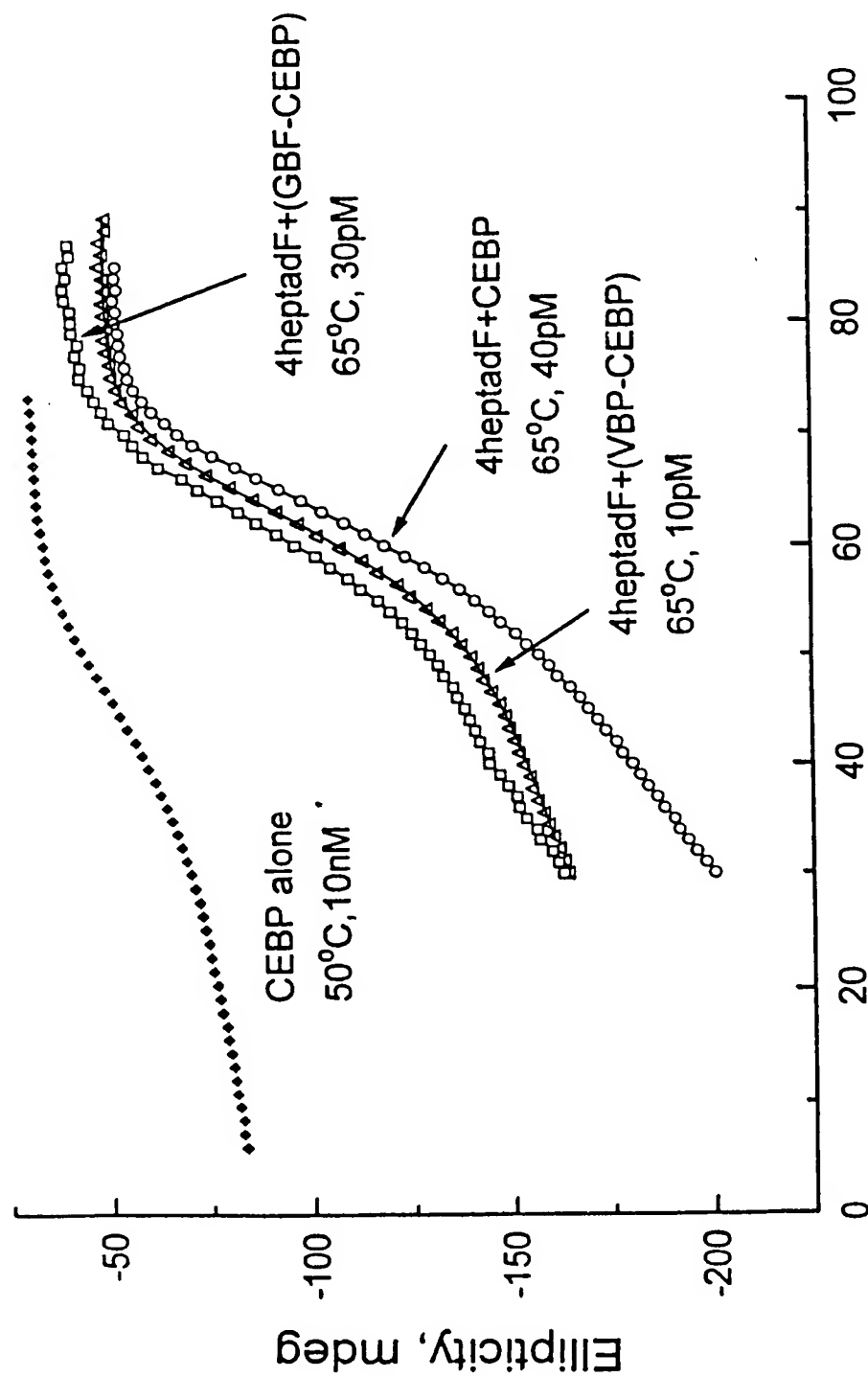


FIG. 2

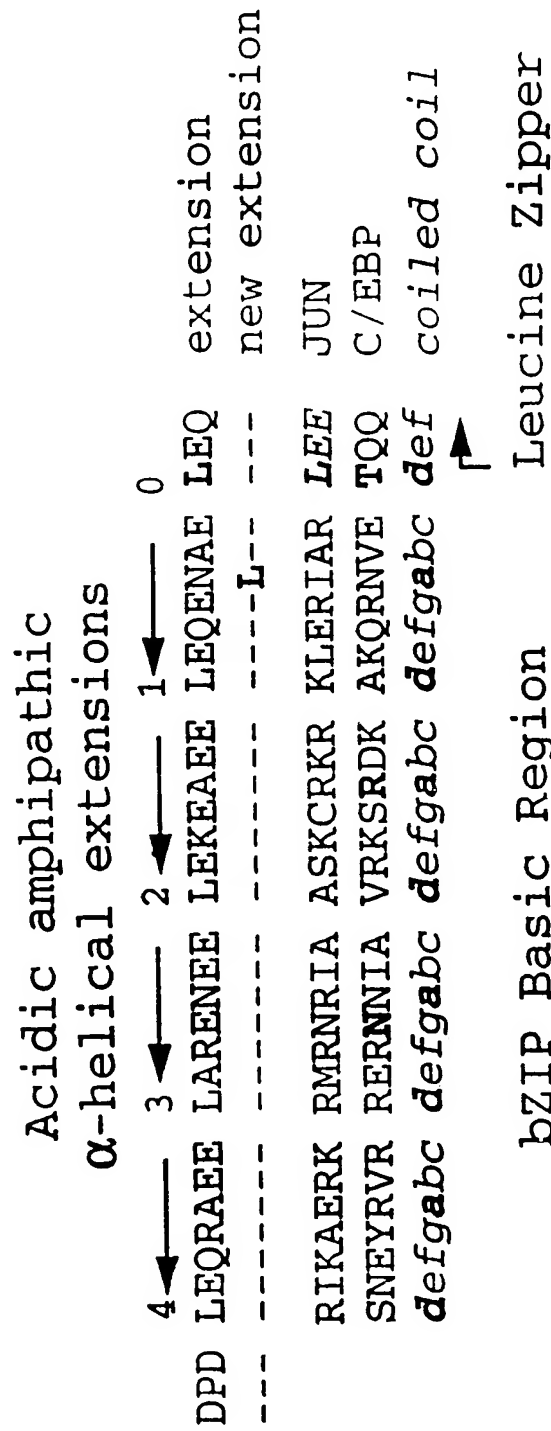


FIG. 3

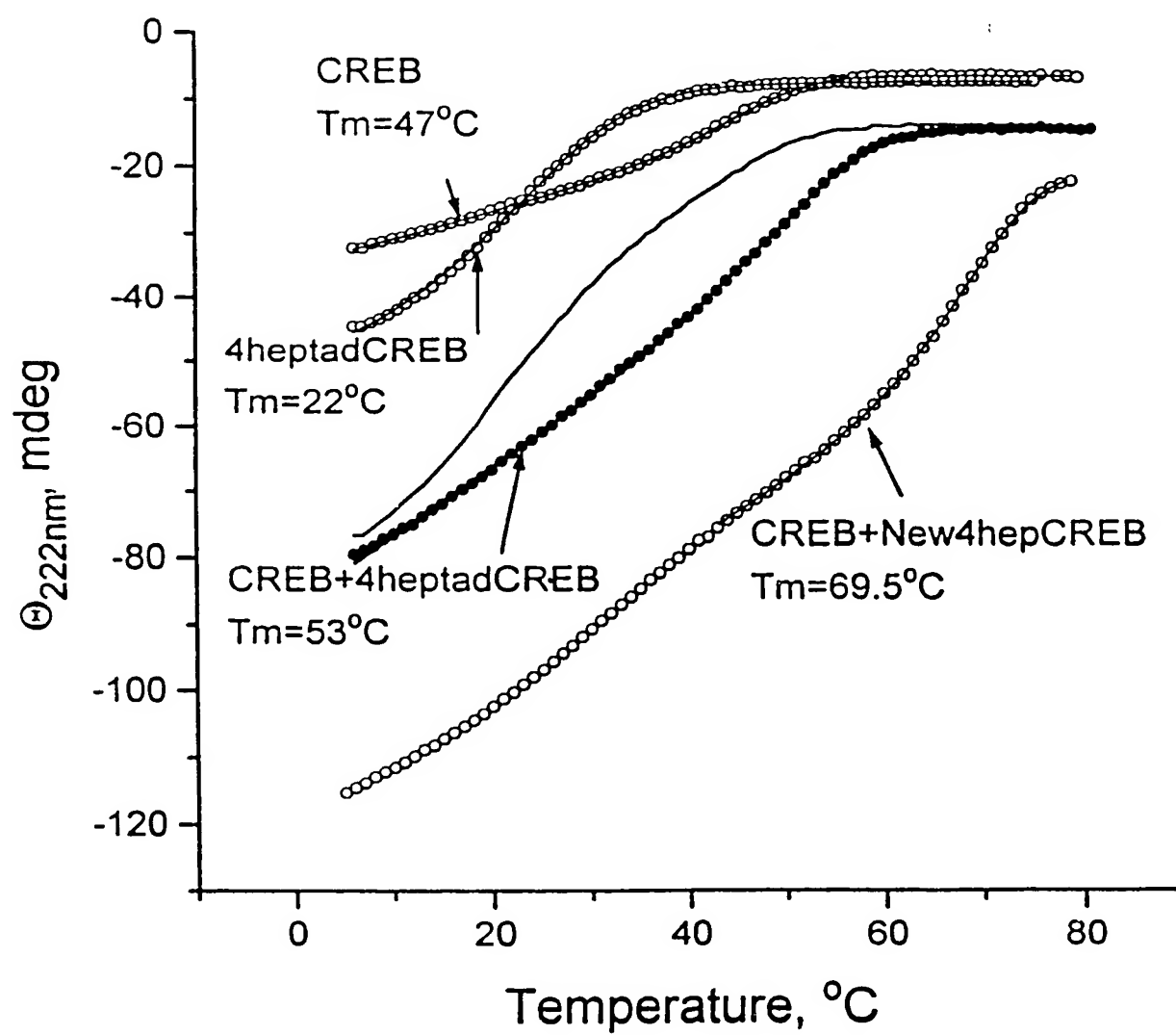


FIG. 4

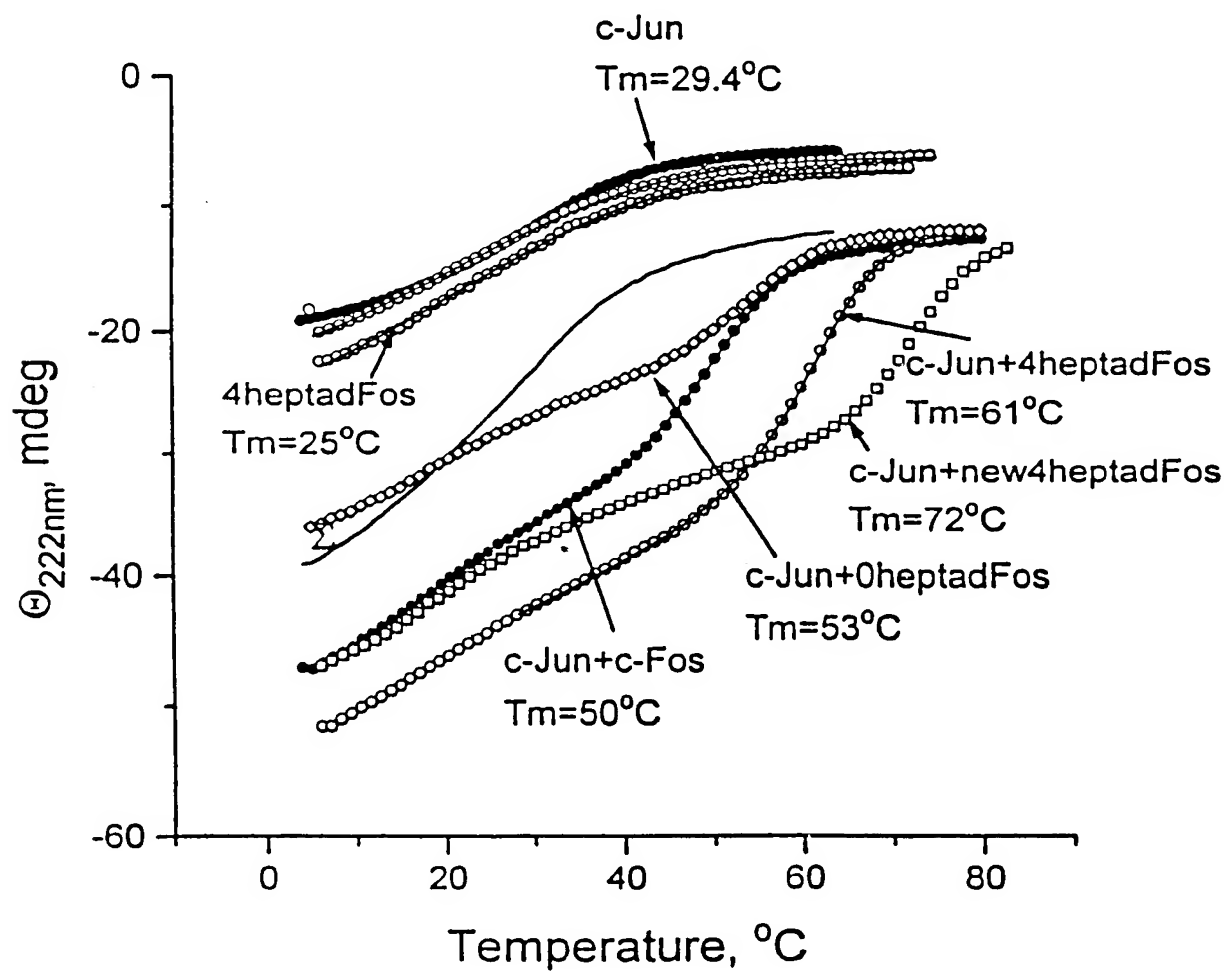


FIG. 5A

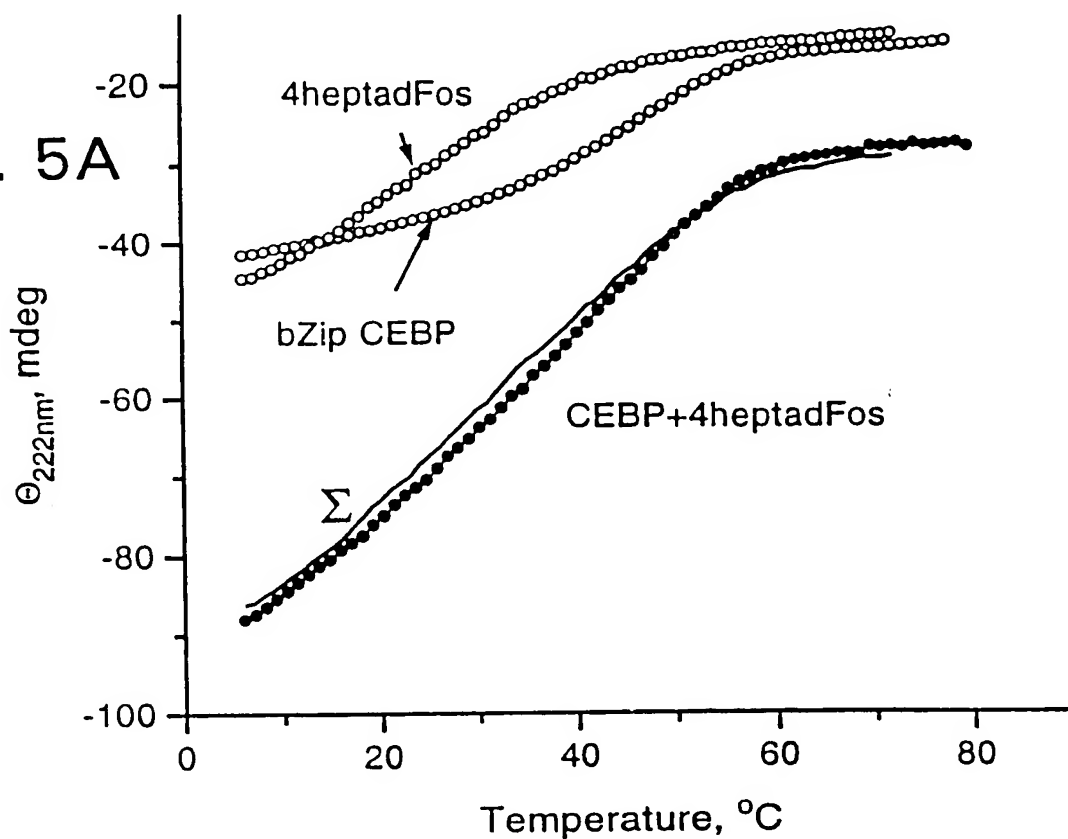


FIG. 5B

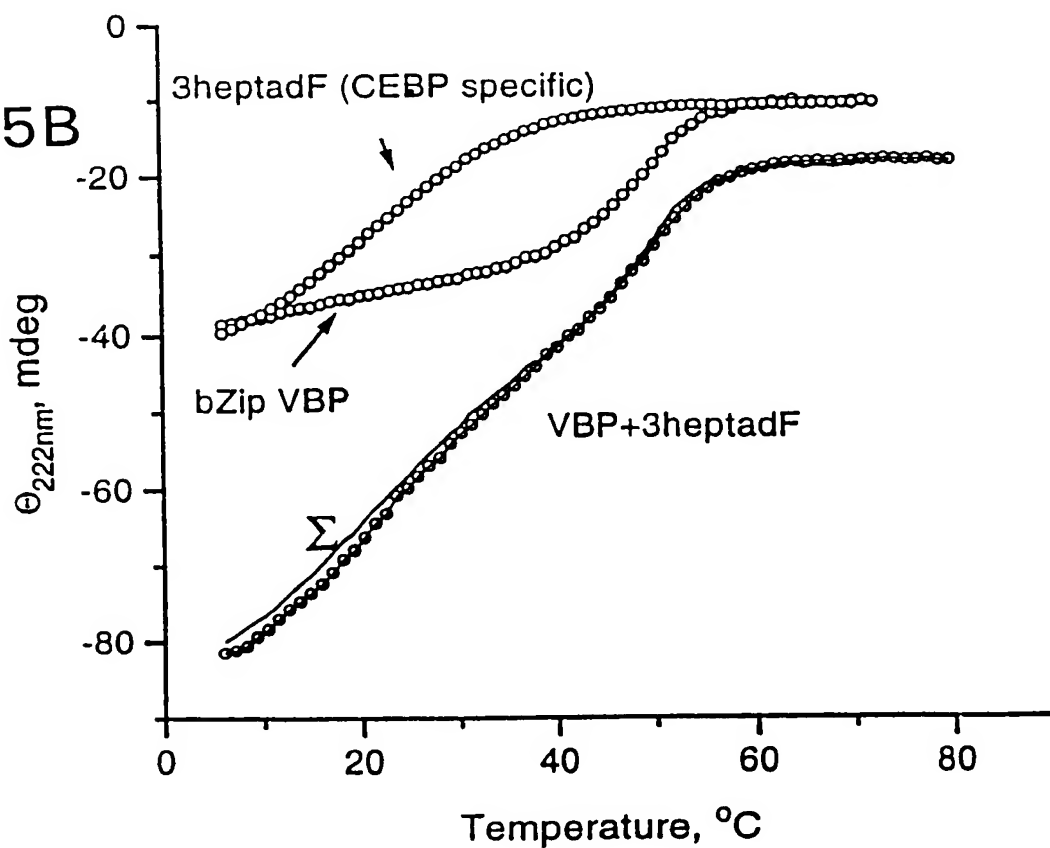


FIG. 6

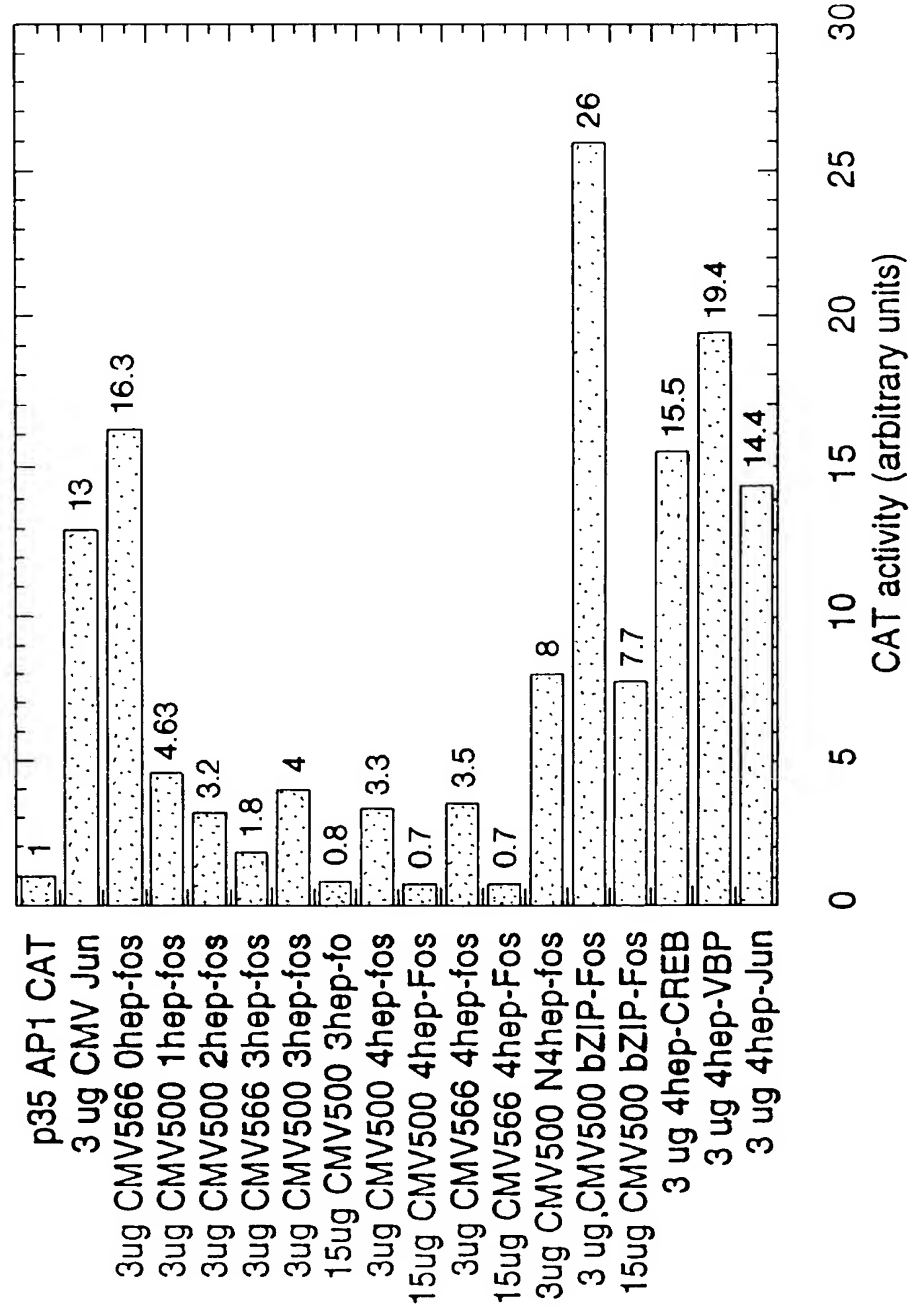
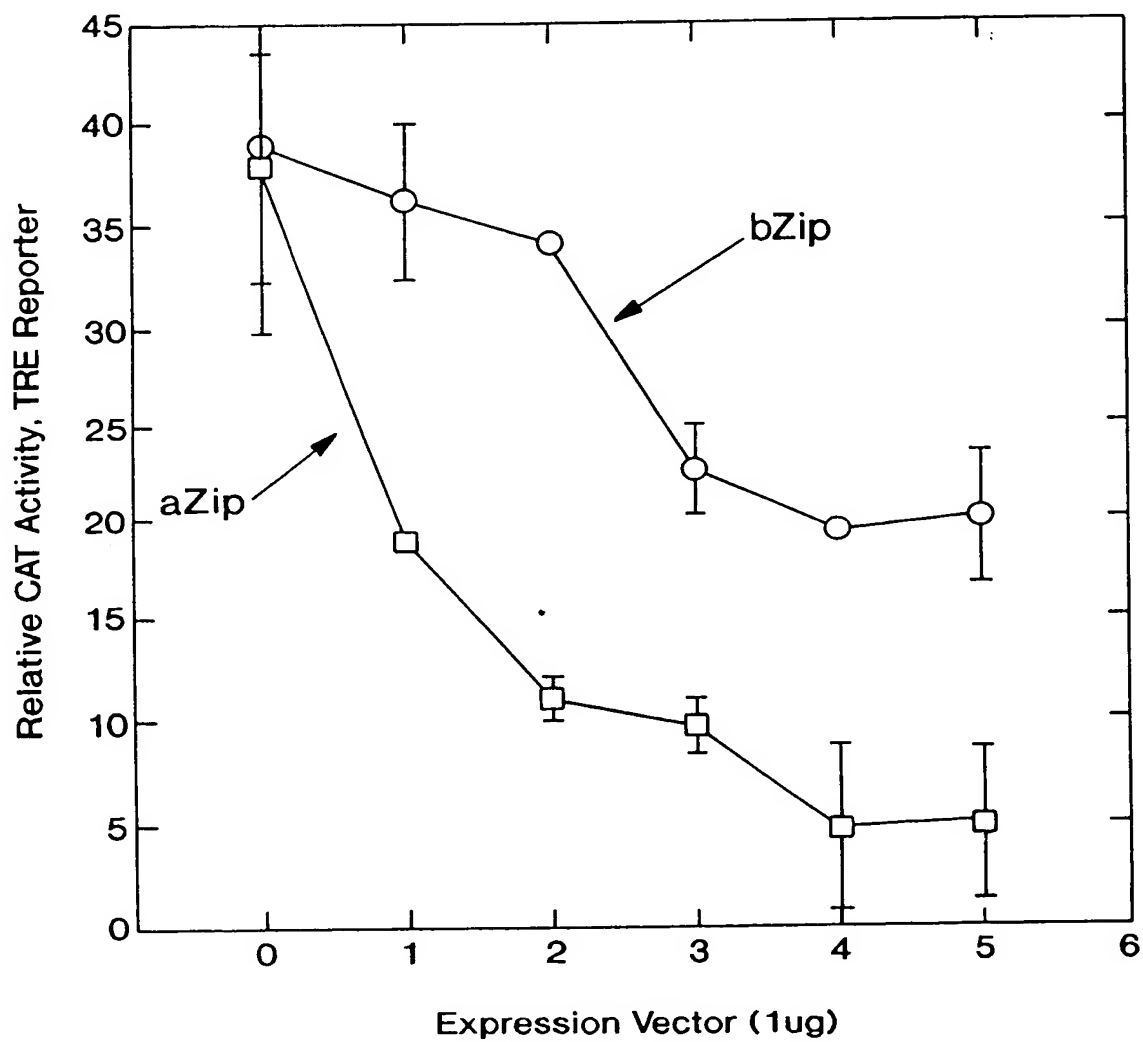


FIG. 7



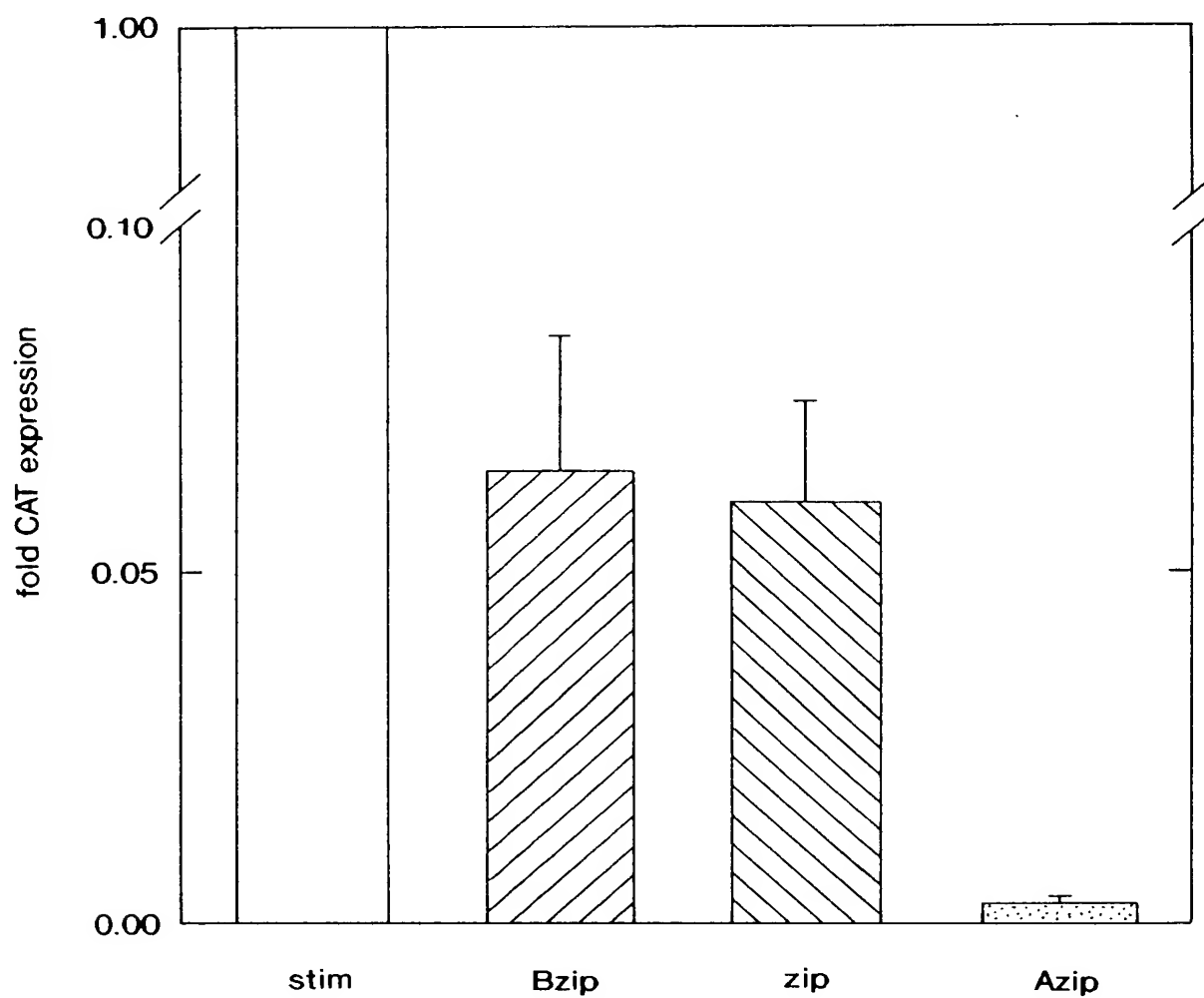


FIG. 8

FIG. 9

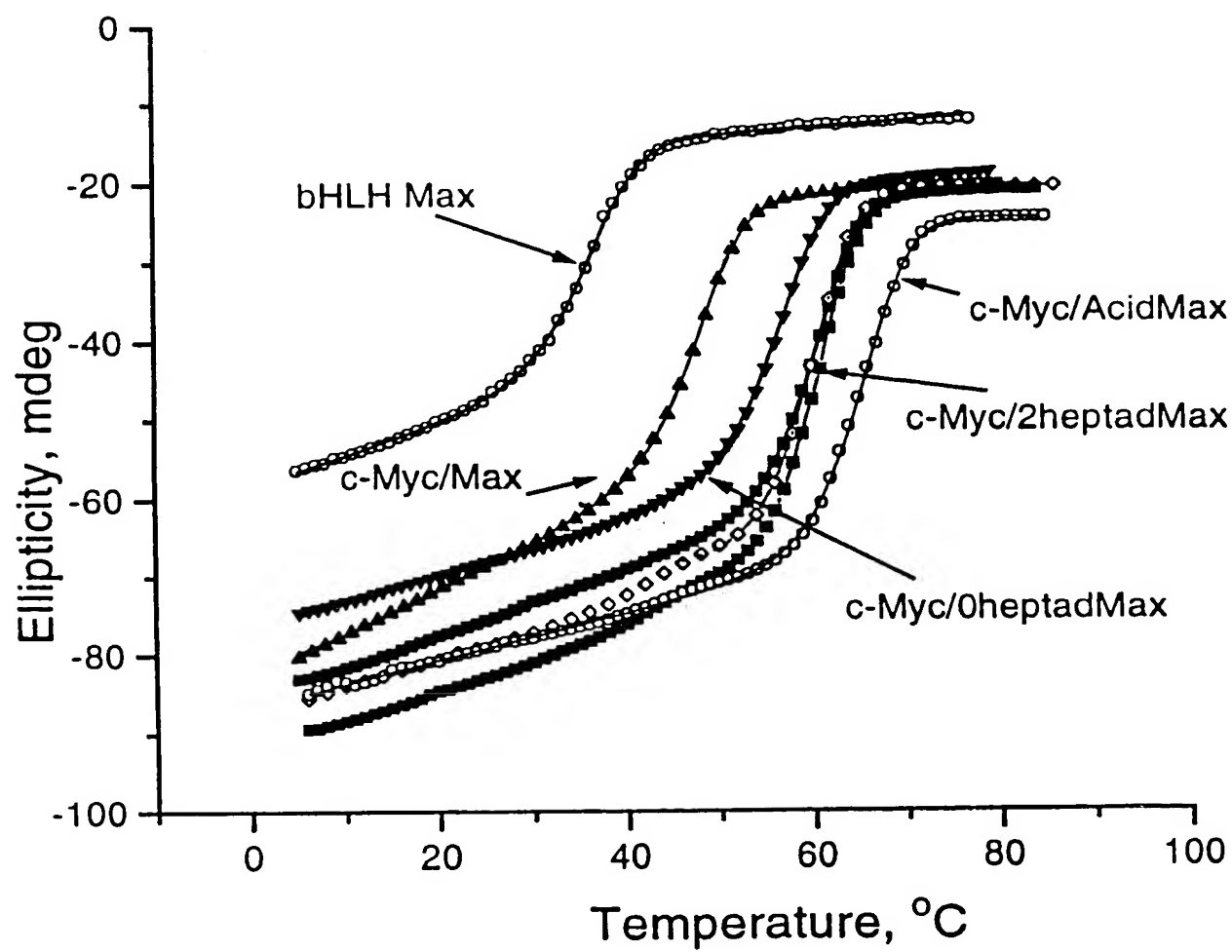


FIG. 10A

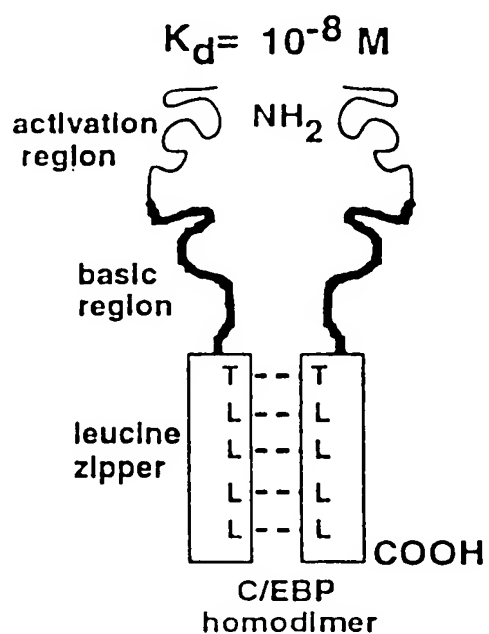
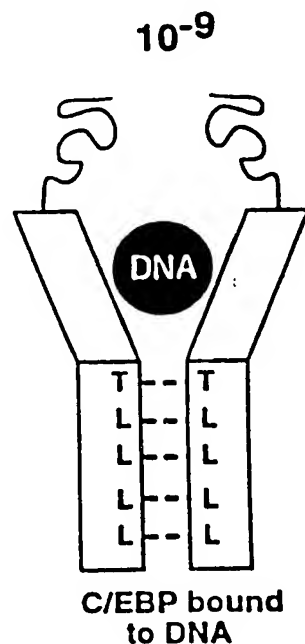


FIG. 10B



7×10^{-9}

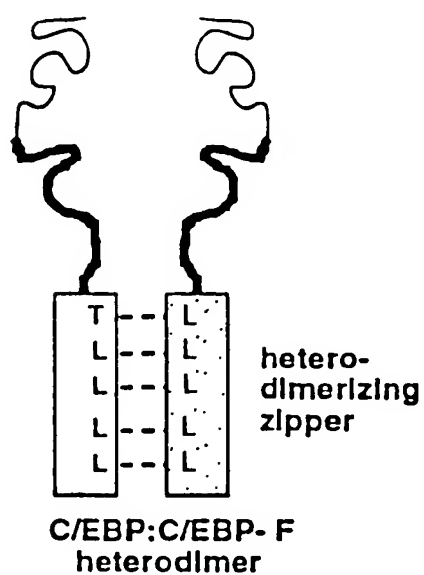


FIG. 10C

3×10^{-9}

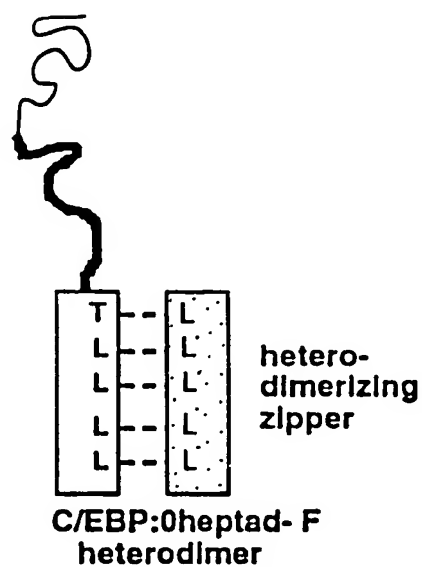


FIG. 10D

FIG. 11A

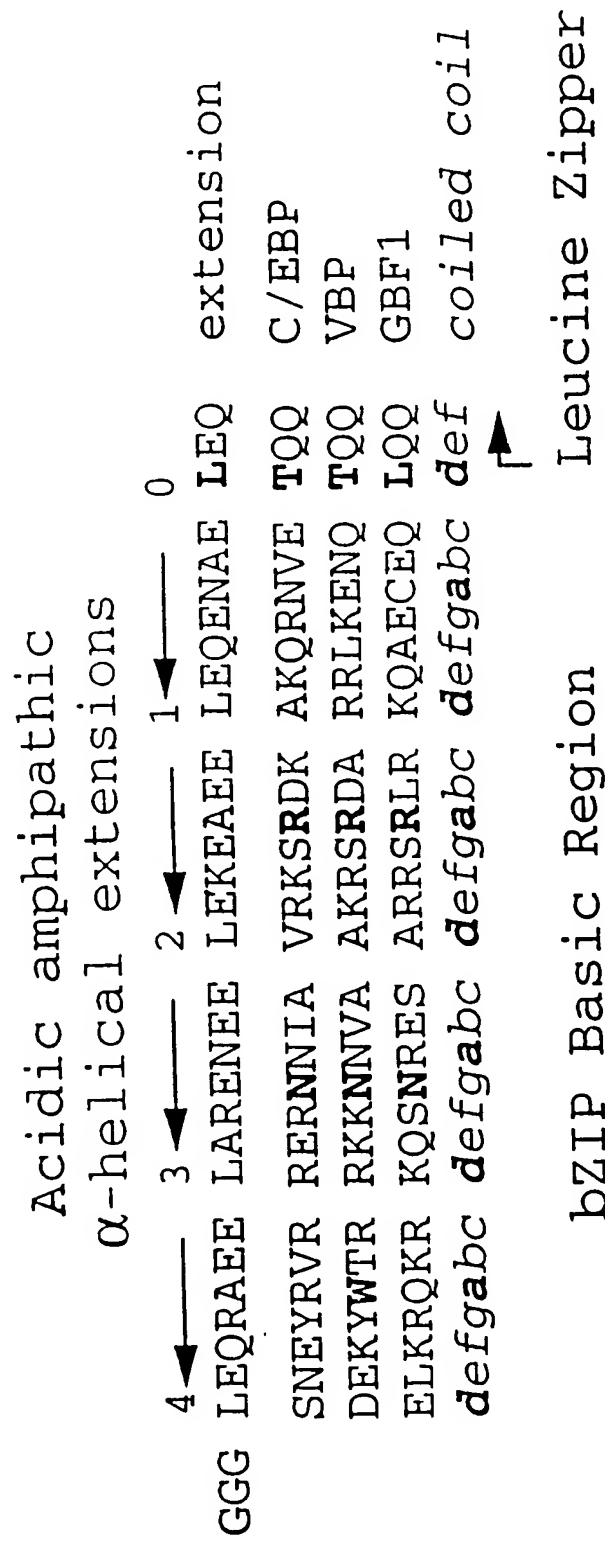


FIG. 11B

bZIP Basic Region

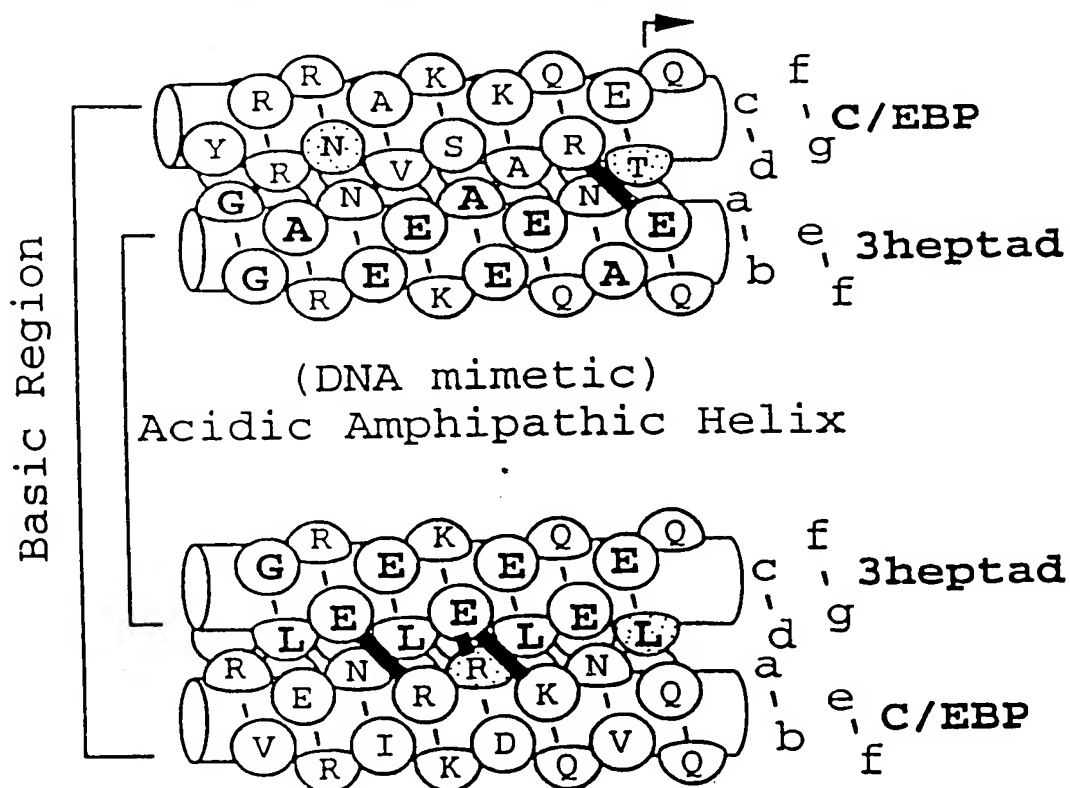


FIG. 11C

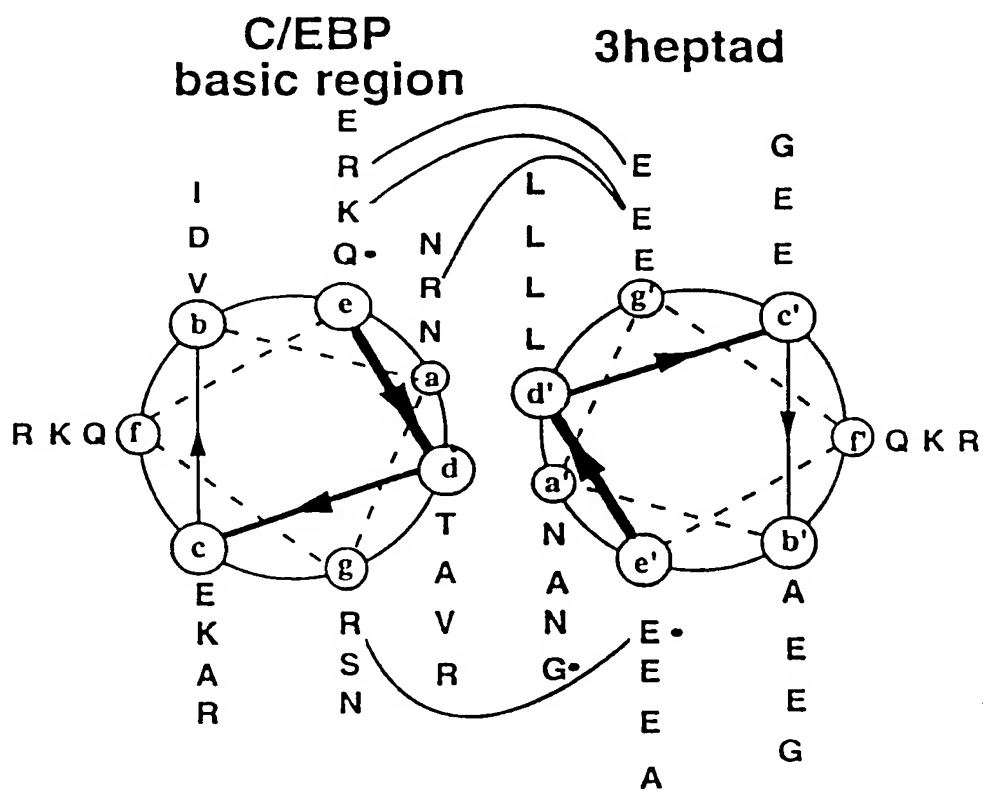


FIG. 12

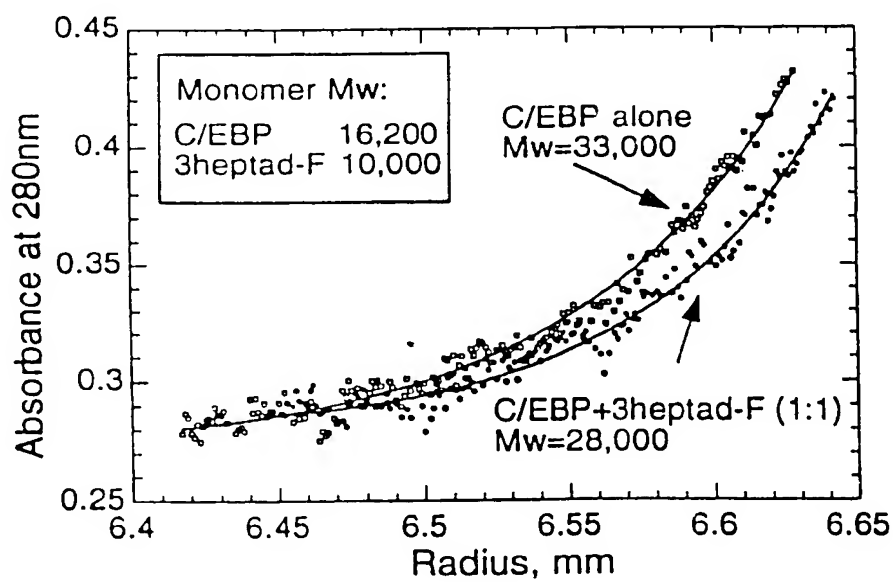


FIG. 13A

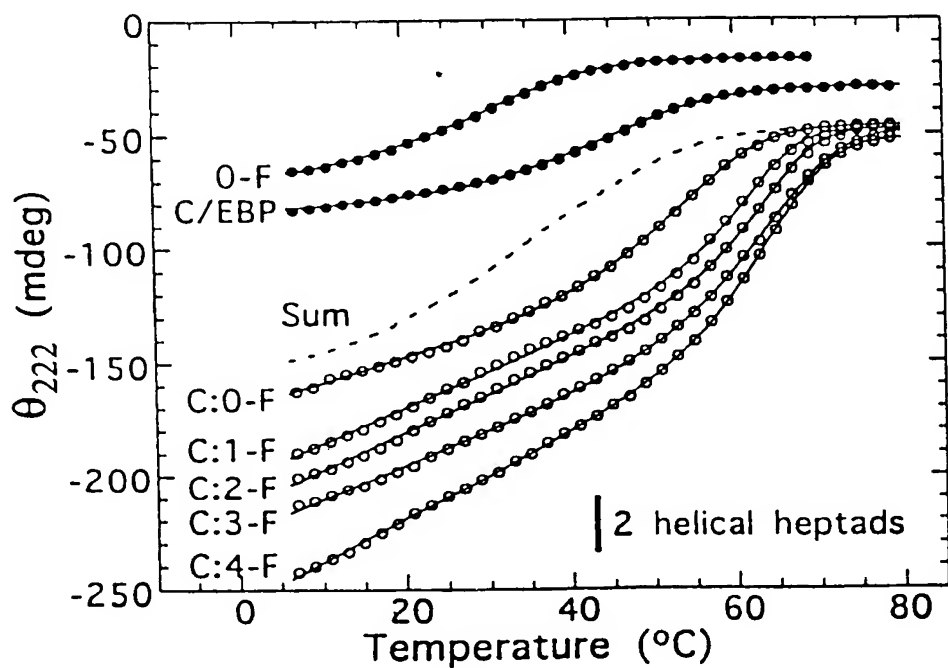
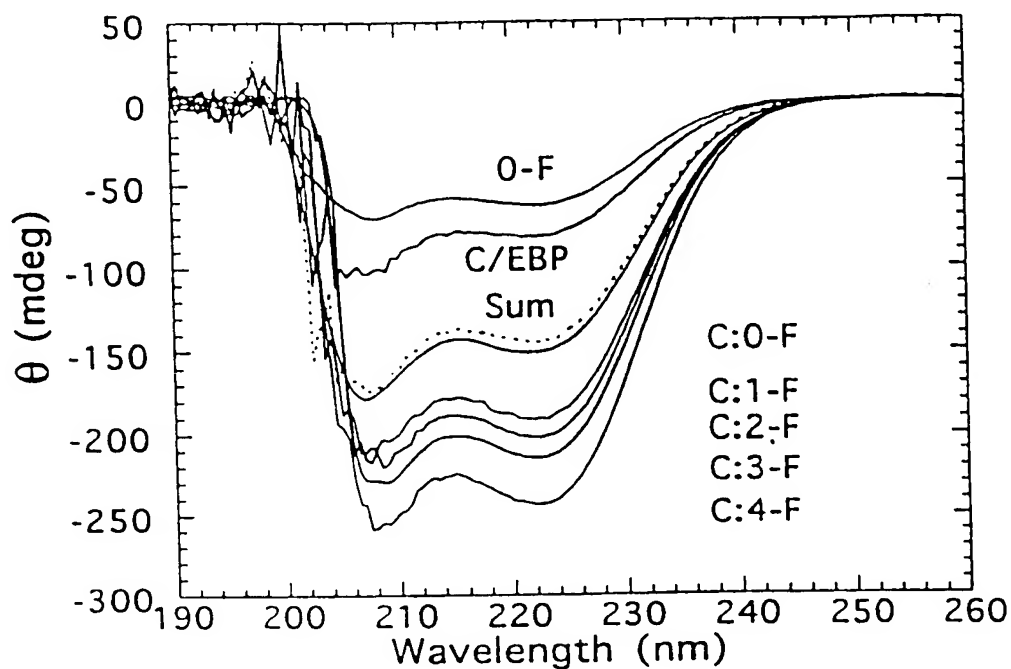


FIG. 13B

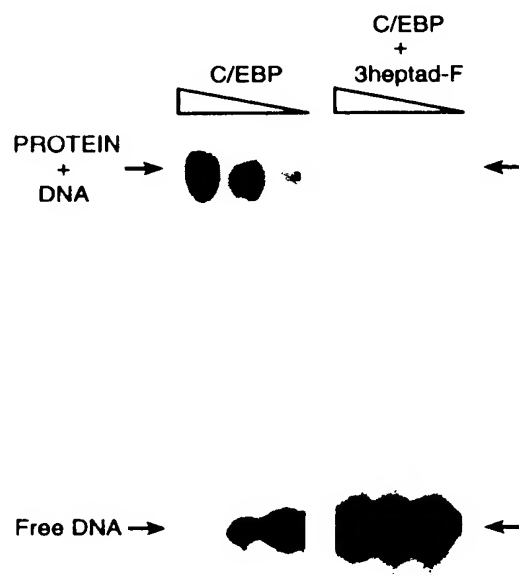


FIG. 14A

FIG. 14B

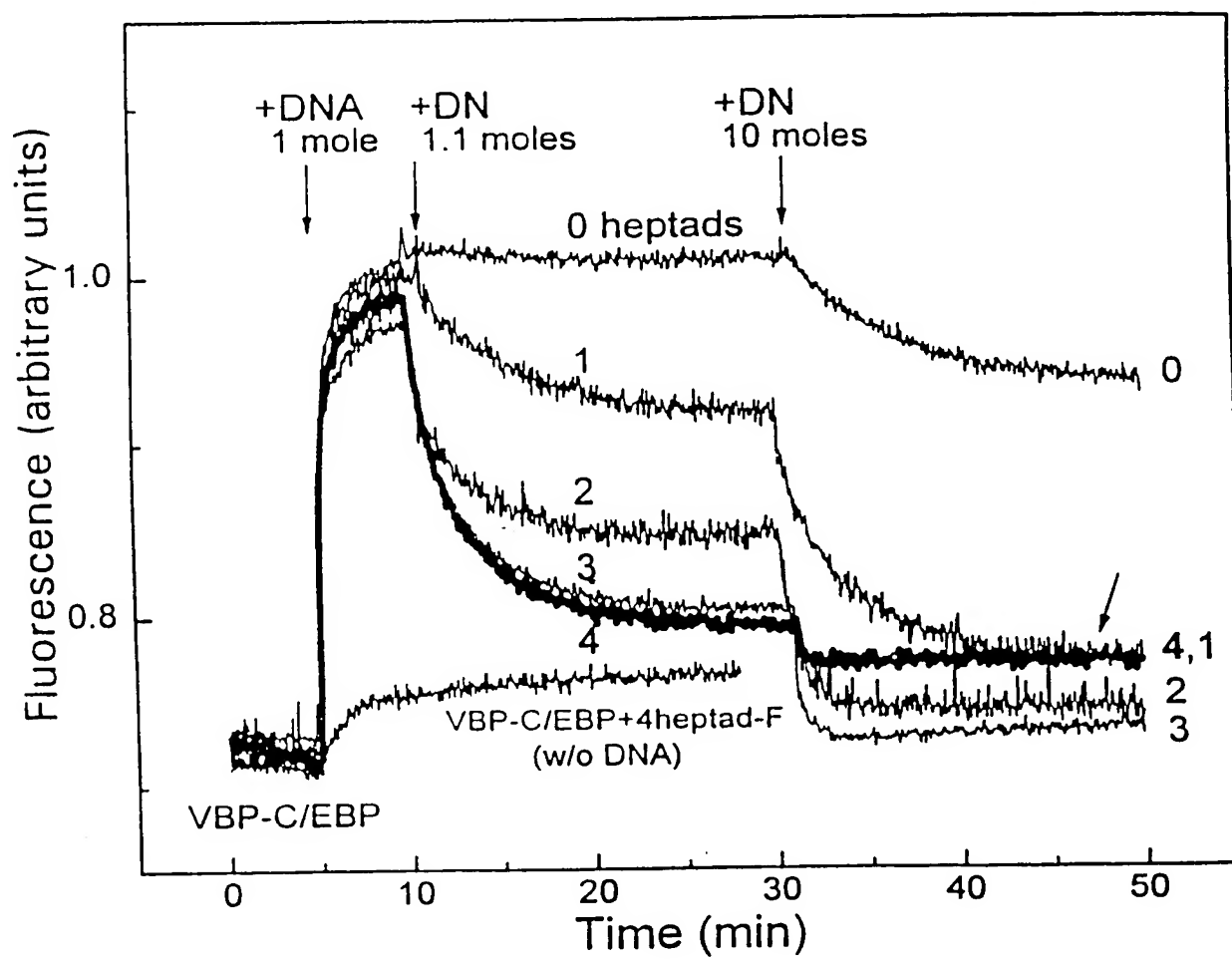


FIG. 15

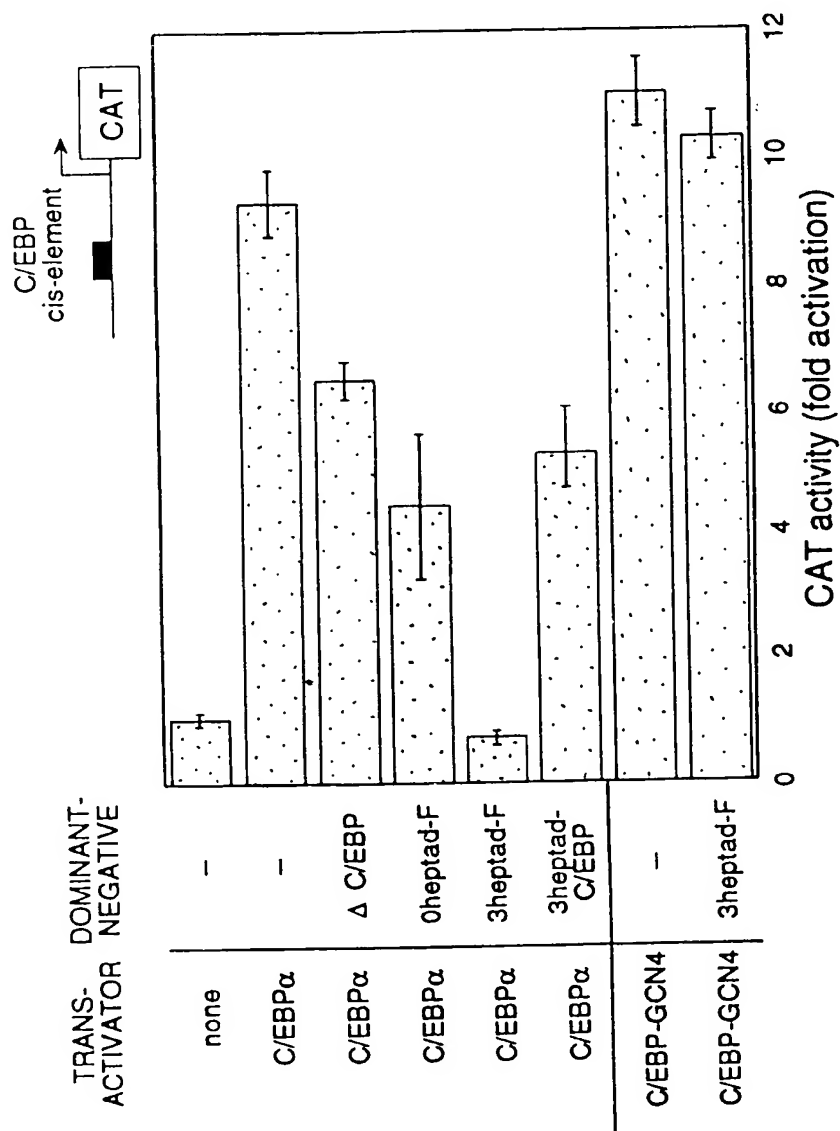


FIG. 16A

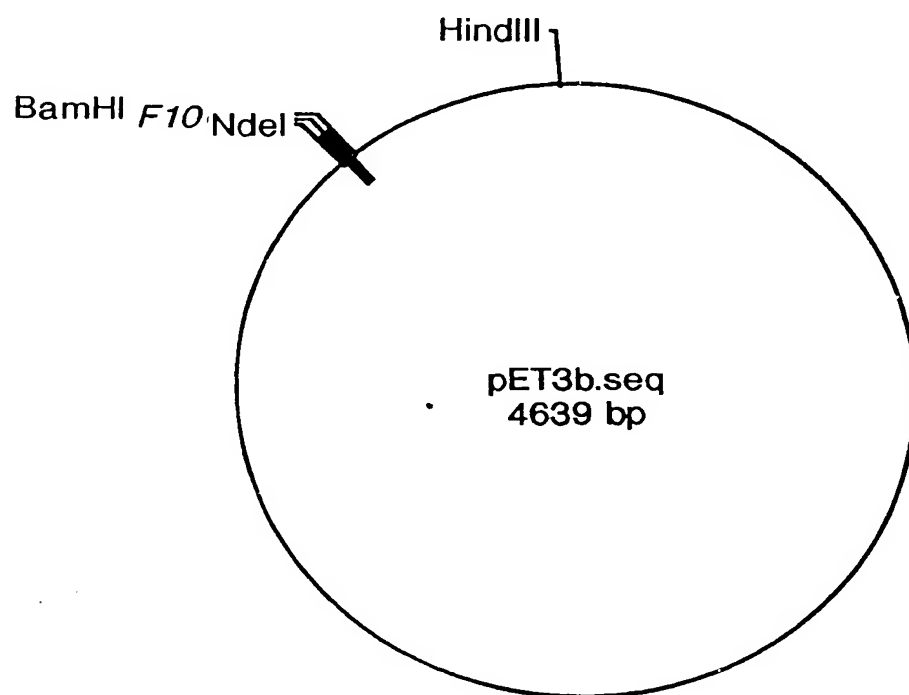


FIG. 16B

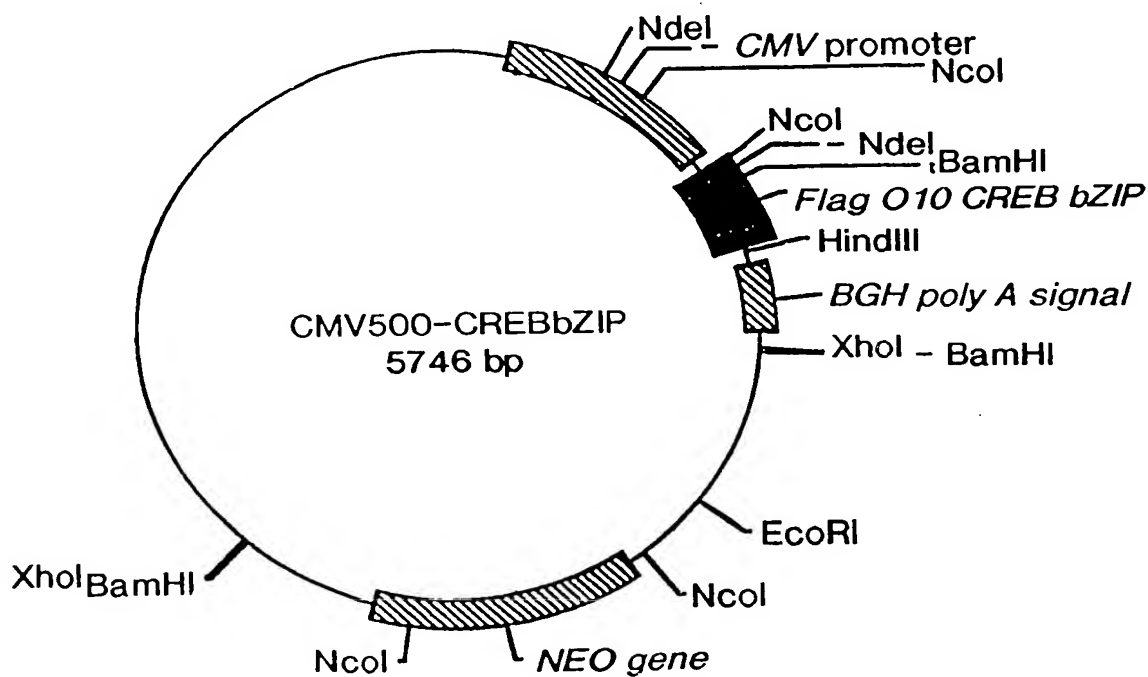
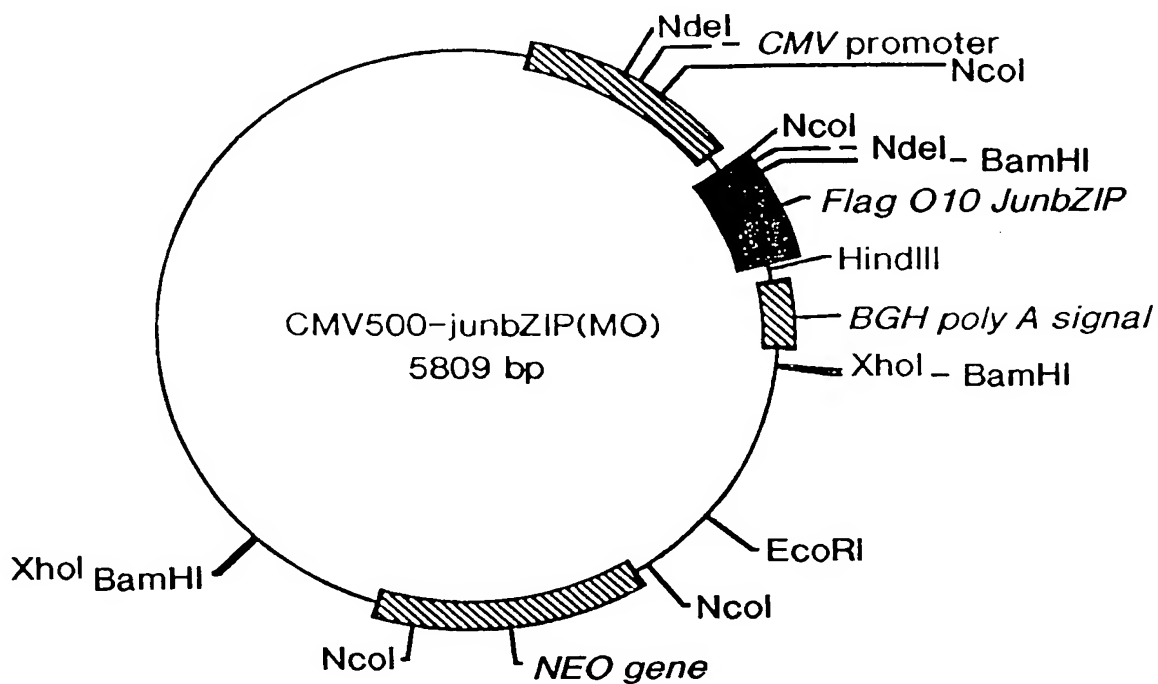


FIG. 16C

```

BamHI
10  * 20 30 40 50
GG ATCCC CTT CCT ACA CAG CCT GCT GAA GAA GCA CGA AAG AGA GAG GTT CGT
L P T Q P A E E A A R K R E V R>
__a__CREB (AA 1-341); NCBI GI: 56005; CODON_START=1; __a__>

60  * 70 80 90 100
CTA ATG AAG AAC AGG GAA GCA GCA AGA GAA TGT CGT AGA AAG AAG AAA
L M K N R E A A R E C R R K K K>
__a__CREB (AA 1-341); NCBI GI: 56005; CODON_START=1; __a__>

110 120 130 140 150
* * * * *
GAA TAT GTG AAA TGT TTA GAG AAC AGA GTG GCA GTG CTT GAA AAC CAA
E Y V K C L E N R V A V L E N Q>
__a__CREB (AA 1-341); NCBI GI: 56005; CODON_START=1; __a__>

160 170 180 190
* * * * *
AAC AAA ACA TTG ATT GAG GAG CTA AAA GCA CTT AAG GAC CTT TAC TGC
N K T L I E E L K A L K D L Y C>
__a__CREB (AA 1-341); NCBI GI: 56005; CODON_START=1; __a__>

200 210
* * * * *
CAC AAG TCA GAT TAA TTC AAG CTT
H K S D *>
__CREB (AA 1-3__>
HindIII

```

FIG. 17

910		920		930		940		D10	
* * *		* * *		* * *		* * *		* * *	
NcoI		GAT		CAT		AGC		ATG	
CC ATG GAC TAC AAG GAC GAC GAT GAC AAG		GAT GAC AAG		CAT ATG GCT		AGC ATG		ACT GGT	
M D Y K D D D D K H M A S M T G>									
950		960		970		980		990	
* * *		* * *		* * *		* * *		* * *	
GGA CAG CAA ATG GGT CGG GAT CCT GAC CTG GAA CAA CGT GCT GAG GAA		GAT GAC AAG		CAT ATG GCT		AGC ATG		ACT GGT	
G Q Q M G R D P D L E Q R A E E>									
1000		1010		1020		1030		1040	
* * *		* * *		* * *		* * *		* * *	
CTG GCC CGT GAA AAC GAA GAG CTG GAA AAA GAG GCC GAA GAG CTG GAG		GAT GAC AAG		CAT ATG GCT		AGC ATG		ACT GGT	
L A R E N E E L E K E A E E L E>									
1050		1060		1070		1080		1090	
* * *		* * *		* * *		* * *		* * *	
CAG GAA CTG GCA GAA CTC GAG AAC AGA GTG GCA GTG CTT GAA AAC CAA		GAT GAC AAG		CAT ATG GCT		AGC ATG		ACT GGT	
Q E L A E L E N R V A V L E N Q>									
1100		1110		1120		1130		1140	
* * *		* * *		* * *		* * *		* * *	
AAC AAA ACA TTG ATT GAG GAG CTA AAA GCA CTT AAG GAC CTT TAC TGC		GAT GAC AAG		CAT ATG GCT		AGC ATG		ACT GGT	
N K T L I E E L K A L K D L Y C>									
1150		1160							
* * *		* * *							
CAC AAG TCA GAT TAA TTC AAG CTT		GAT GAC AAG		CAT ATG GCT		AGC ATG		ACT GGT	
H K S D * F [K L>]									

FIG. 19

Hind III

BamH I 10 20 30 40
 * * * * *
 GGATCCC AAG GTG GAA CAG TTA TCT CCA GAA GAA GAA GAG AAA AGG AGA
 P D K V E Q> L S P E E E E K R R>
 ____1783 TO ____> ____2470_2466 TO 2573 OF HUM FOS _0__b____>

50 60 70 80 90
 * * * * * *
 ATC CGA AGG GAA AGG AAT AAG ATG GCT GCA GCC AAA TGC CGC AAC CGG
 I R R E R N K M A A A K C R N R>
 ____2500_b____b____251_2466 TO 2573 OF HUM FOS _30_b____b____2540b____>

100 110 120 130 140
 * * * * * *
 AGG AGG GAG CTG ACT GAT ACA CTC CAA GCG GAG ACA GAC CAA CTA GAA
 R R E L T D T L Q A> E T D Q L E>
 ____b_2_2466 TO 2573 OF HUM FOS _570b____> 26_2688 TO 3329 OF H____>

150 160 170 180 190
 * * * * * *
 GAT GAG AAG TCT GCT TTG CAG ACC GAG ATT GCC AAC CTG CTG AAG GAG
 D E K S A L Q T E I A N L L K E>
 ____2710_c____c____272_2688 TO 3329 OF HUM FOS _40_c____c____2750c____>

200 210 220 230 240
 * * * * * *
 AAG GAA AAA CTA GAG TTC ATC CTG GCA GCT CAC CGA CCT GCC TGC AAG
 K E K L E F I L A A H R P A C K>
 ____c_2760__c____c____2688 TO 3329 OF HUM FOS _2790__c____c____2800_>

250 260
 * * *
 ATC CCT GAT TAATTCAAGC TT
 I P> Hind III
 ____c____>

FIG. 20

900 * NcoI Flag NdeI $\Phi 10$

CC ATG GAC TAC AAG GAC GAC GAT GAC AAG CAT ATG GCT AGC ATG ACT GGT GGA CAG CAA ATG

M D Y K D D D D K D K H M A S M T G G Q Q M>

960 * BamHI

GGT CGG GAT CCC AAG GTG GAA CAG TTA TCT CCA GAA GAA GAG AAA AGG AGA ATC CGA

G R D P K V E Q L S P E E E E K R I R>

1020 Fos b zip

AGG GAA AGG AAT AAG ATG GCT GCA GCC AAA TGC CGC AAC CGG AGG AGG GAG CTG ACT GAT

R E R N K M A A A K C R N R R E L T D>

1080 *

ACA CTC CAA GCG GAG ACA GAC CAA CTA GAA GAT GAG AAG TCT GCT TTG CAG ACC GAG ATT

T L Q A E T D Q L E D E K S A L Q T E I>

1140 *

GCC AAC CTG CTG AAG GAG AAG GAA AAA CTA GAG TTC ATC CTG GCA GCT CAC CGA CCT GCC

A N L L K E K E K L E F I L A A H R P A>

1200 * HindIII

TGC AAG ATC CCT GAT TAA GCCTT

C K I P D *>

FIG. 21

FIG. 22

```

>NdeI
|
* 10      20      30      40      50
*  *      *      *      *      *
ATATACAT ATG GCT AGC ATG ACT GGT GGA CAG CAA ATG GGT CGG GAT CCT
      M  A  S  M  T  G  G  Q  Q  M  G  R>
      _a_a_a_a_a_F10_a_a_a_a_a_>
                                     D  P>
                                     _b_>

      60      70      80      90
      *      *      *      *
GAC CTG GAA CAA CGT GCT GAG GAA CTG GCC CGT GAA AAC GAA GAG CTG
D  L  E  Q  R  A  E  E  L  A  R  E  N  E  E  L>
_b_b_b_b_4HEPTAD ACIDIC EXTENSION_b_b_b_b_>

                                     >XhoI
                                     |
100      110      120      130      140
*      *      *      *      *
GAA AAA GAG GCC GAA GAG CTG GAG CAG GAA AAC GCT GAA CTC GAG GCG
E  K  E  A  E  E  L  E  Q  E  N  A  E  L  E>
_b_b_b_b_4HEPTAD ACIDIC EXTENSION_b_b_b_b_>
                                     A>
                                     _>

      150      160      170      180      190
      *      *      *      *      *
GAG ACA GAC CAA CTA GAA GAT GAG AAG TCT GCT TTG CAG ACC GAG ATT
E  T  D  Q  L  E  D  E  K  S  A  L  Q  T  E  I>
_c_c_c_c_c_C-FOS PROTEIN_c_c_c_c_c_>

      200      210      220      230      240
      *      *      *      *      *
GCC AAC CTG CTG AAG GAG AAG GAA AAA CTA GAG TTC ATC CTG GCA GCT
A  N  L  L  K  E  K  E  K  L  E  F  I  L  A  A>
_c_c_c_c_c_C-FOS PROTEIN_c_c_c_c_c_>

                                     >HindIII
                                     |
      250      260      270      280
      *      *      *      *
CAC CGA CCT GCC TGC AAG ATC CCT GATT AATTC AAGCT T
H  R  P  A  C  K  I  P>
_c_C-FOS PROTEIN_c_c_>

```

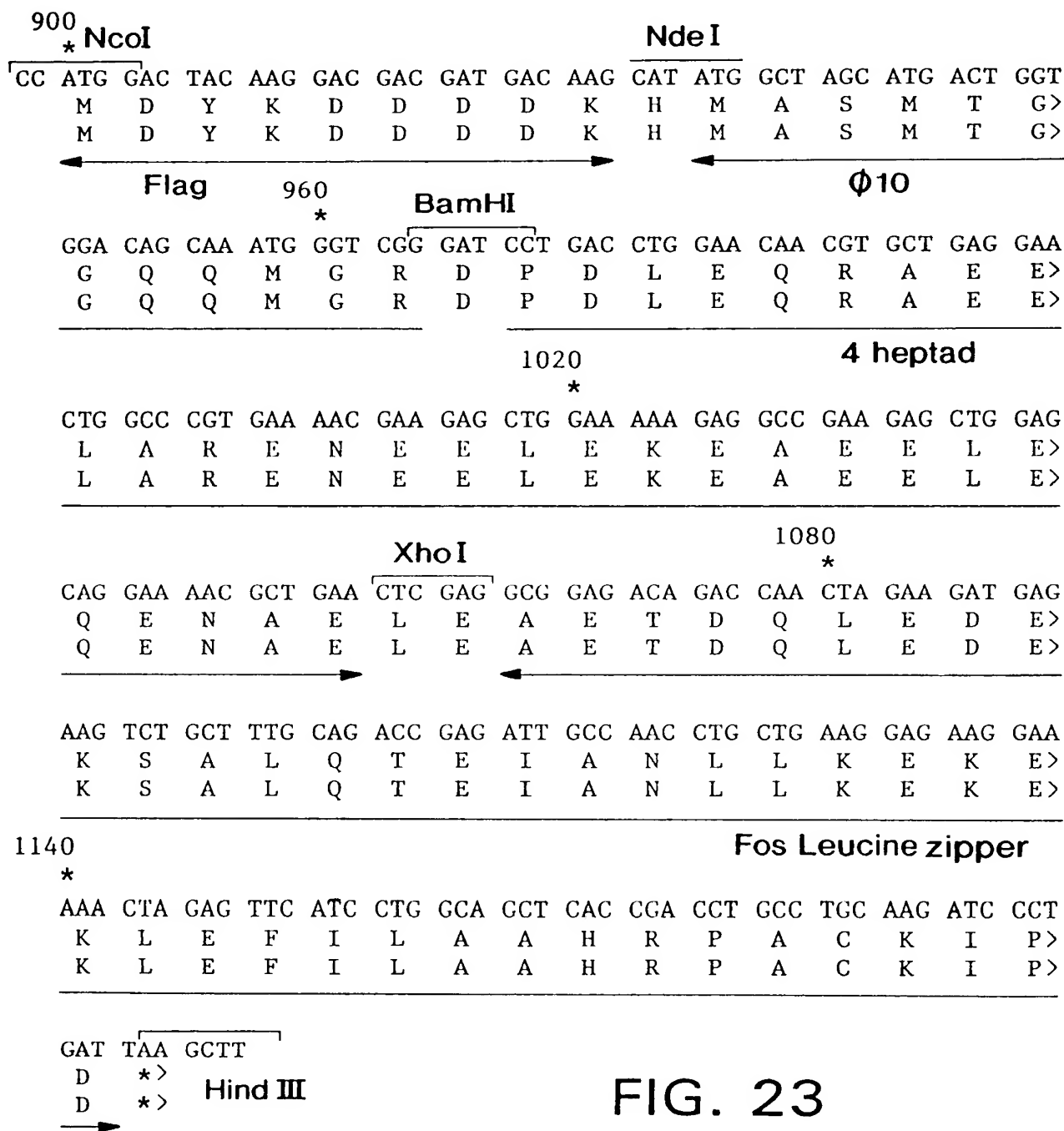


FIG. 23

900 * NcoI Flag NdeI Ø10
 CC ATG GAC TAC AAG GAC GAC GAT GAC AAG CAT ATG GCT AGC ATG ACT GGT GGA CAG CAA ATG
 M D Y K D D D D K H M A S M T G G Q Q M>

960 * BamHI
 GGT CGG GAT CCC TCC CCT ATT GAC ATG GAG TCG CAG GAG AGA ATC AAA GCC GAG AGA AAA
 G R D P S P I D M E S Q E R I K A E R K>

1020 * Jun b zip
 CGC ATG AGA AAC AGA ATT GCG GCG TCC AAA TGC CGG AAA AGG AAG TTG GAA AGG ATT GCC
 R M R N R I A A S K C R K R K L E R I A>

1080 *
 AGG TTG GAA GAA AAA GTG AAA ACT TTG AAA GCC CAG AAC TCA GAG CTG GCA TCC ACG GCC
 R L E E K V K T L K A Q N S E L A S T A>

1140 *
 AAC ATG CTC AGA GAA CAG GTT GCA CAG CTT AAG CAG AAG GTC ATG AAC CAT GTC AAC AGC
 N M L R E Q V A Q L K Q K V M N H V N S>

1200 * HdIII
 GGG TGC CAG CTA ATG CTA ACA CAA CAG TTG CAA ACG TTT TGA TTC AAGCTT
 G C Q L M L T Q Q Q L Q T F * F>

FIG. 24

FIG. 25

```

>NdeI
|
4090      4100      4110      4120      4130
* | *      *      *      *      *
ATACAT ATG GCT AGC ATG ACT GGT GGA CAG CAA ATG GGT CGG GAT CCC GAC
  M   A   S   M   T   G   G   Q   Q   M   G   R>
  _a_ _a_ _a_ _a_ _a_ F10 _a_ _a_ _a_ _a_ _a_ >
                                     D   P   D>
                                     _b_ _b_ >

>XhoI
|
4140      4150      4160      4170      4180
* | *      *      *      *      *
GAA GAG GAA GAT GAC GAA GAA GAA CTC GAG GAA CTG GAA GAC AGC TTT
  E   E   E   D   D   E   E   E   L   E   E   L   E>
  _b_ _b_ _b_ _b_ _b_ POLY-GLU _b_ _b_ _b_ _b_ _b_ >
                                     D   S   F>
                                     _c_ _c_ >

4190      4200      4210      4220      4230
* | *      *      *      *      *
CAC AGT TTG CGG GAC TCA GTC CCA TCA CTC CAA GGA GAG AAG GCA TCC
  H   S   L   R   D   S   V   P   S   L   Q   G   E   K   A   S>
  _c_ _c_ _c_ _c_ _c_ MAX BHLH DOMAIN _c_ _c_ _c_ _c_ _c_ >

4240      4250      4260      4270
* | *      *      *      *      *
CGG GCC CAA ATC CTA GAC AAA GCA ACA GAG TAT ATC CAG TAT ATG CGA
  R   A   Q   I   L   D   K   A   T   E   Y   I   Q   Y   M   R>
  _c_ _c_ _c_ _c_ _c_ MAX BHLH DOMAIN _c_ _c_ _c_ _c_ _c_ >

4280      4290      4300      4310      4320
* | *      *      *      *      *
AGG AAA AAC CAT ACG CAC CAG CAA GAC ATT GAT GAC CTC AAG CGG CAG
  R   K   N   H   T   H   Q   Q   D   I   D   D   L   K   R   Q>
  _c_ _c_ _c_ _c_ _c_ MAX BHLH DOMAIN _c_ _c_ _c_ _c_ _c_ >

4330      4340      4350      4360      4370
* | *      *      *      *      *
AAT GCT CTT CTG GAG CAA CAA GTC CGT GCA CTG GAG AAG GCA AGA TCA
  N   A   L   L   E   Q   Q   V   R   A   L   E   K   A   R   S>
  _c_ _c_ _c_ _c_ _c_ MAX BHLH DOMAIN _c_ _c_ _c_ _c_ _c_ >

>HindIII
|
4380      4390      4400
* | *      *      *
AGT GCC CAA CTG CAG ACC TGAGGCAA GCTTATC
  S   A   Q   L   Q   T>
  _MAX BHLH DOMAIN _c_ >

```

FIG. 26

```

>NdeI
|
4090          4100          4110          4120          4130
* | *          *          *          *          *
ATATACAT ATG GCT AGC ATG ACT GGT GGA CAG CAA ATG GGT CGG GAT CCT
      M  A  S  M  T  G  G  Q  Q  M  G  R>
      _a_a_a_a_a_a_F10_a_a_a_a_a_a_>
                                     D  P>
                                     _b_>

                                     >XhoI
                                     |
4140          4150          4160          4170
* | *          *          *          *          *
GAC CTG GAA AAA GAG GCC GAA GAG CTG GAG CAG GAA AAC GCT GAA CTC
D  L  E  K  E  A  E  E  L  E  Q  E  N  A  E  L>
_b_b_TWO AMPHIPATHIC HEPTAD S (1st PHASE- 783) _b_b_>

4180          4190          4200          4210          4220
* | *          *          *          *          *
GAG CTG GAA GAC AGC TTT CAC AGT TTG CGG GAC TCA GTC CCA TCA CTC
E  L  E>
_b_b_>
      D  S  F  H  S  L  R  D  S  V  P  S  L>
      _c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_>

4230          4240          4250          4260          4270
* | *          *          *          *          *
CAA GGA GAG AAG GCA TCC CGG GCC CAA ATC CTA GAC AAA GCA ACA GAG
Q  G  E  K  A  S  R  A  Q  I  L  D  K  A  T  E>
_c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_>

4280          4290          4300          4310          4320
* | *          *          *          *          *
TAT ATC CAG TAT ATG CGA AGG AAA AAC CAT ACG CAC CAG CAA GAC ATT
Y  I  Q  Y  M  R  R  K  N  H  T  H  Q  Q  D  I>
_c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_>

4330          4340          4350          4360          4370
* | *          *          *          *          *
GAT GAC CTC AAG CGG CAG AAT GCT CTT CTG GAG CAA CAA GTC CGT GCA
D  D  L  K  R  Q  N  A  L  L  E  Q  Q  V  R  A>
_c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_>

                                     >HindIII
                                     |
4380          4390          4400          4410          4420
* | *          *          *          *          *
CTG GAG AAG GCA AGA TCA AGT GCC CAA CTG CAG ACC TGA GGCAAGCTTA
L  E  K  A  R  S  S  A  Q  L  Q  T>
_c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_>

```

FIG. 27

```

>NdeI
|
4090          4100          4110          4120          4130
* | * * * * *
ATATACAT ATG GCT AGC ATG ACT GGT GGA CAG CAA ATG GGT CGG GAT CCT
  M  A  S  M  T  G  G  Q  Q  M  G  R>
  _a_a_a_a_a_F10_a_a_a_a_a_>
                                     D  P>
                                     _b_>

                                     >XhoI
                                     |
4140          4150          4160          4170
* | * * * * *
GAC CTG GAA AAA GAG GCC GAA GAG CTG GAG CAG GAA AAC GCT GAA CTC
  D  L  E  K  E  A  E  E  L  E  Q  E  N  A  E  L>
  _b_b_TWO AMPHIPATHIC HEPTAD S (2ND PHASE- 784)_b_b_>

4180          4190          4200          4210          4220
* | * * * * *
GAG GAA CTG GAA GAC AGC TTT CAC AGT TTG CGG GAC TCA GTC CCA TCA
  E  E  L  E>
  _TWO AMPH_>
                                     D  S  F  H  S  L  R  D  S  V  P  S>
                                     _c_c_c_MAX BHLH DOMAIN_c_c_c_c_>

4230          4240          4250          4260          4270
* | * * * * *
CTC CAA GGA GAG AAG GCA TCC CGG GCC CAA ATC CTA GAC AAA GCA ACA
  L  Q  G  E  K  A  S  R  A  Q  I  L  D  K  A  T>
  _c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_>

4280          4290          4300          4310          4320
* | * * * * *
GAG TAT ATC CAG TAT ATG CGA AGG AAA AAC CAT ACG CAC CAG CAA GAC
  E  Y  I  Q  Y  M  R  R  K  N  H  T  H  Q  Q  D>
  _c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_>

4330          4340          4350          4360          4370
* | * * * * *
ATT GAT GAC CTC AAG CGG CAG AAT GCT CTT CTG GAG CAA CAA GTC CGT
  I  D  D  L  K  R  Q  N  A  L  L  E  Q  Q  V  R>
  _c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_>

                                     >HindIII
                                     |
4380          4390          4400          4410          4420
* | * * * * *
GCA CTG GAG AAG GCA AGA TCA AGT GCC CAA CTG CAG ACC TGAGGCAAGC
  A  L  E  K  A  R  S  S  A  Q  L  Q  T>
  _c_c_c_c_c_MAX BHLH DOMAIN_c_c_c_c_c_>

*
TTATC

```

FIG. 28

```

>NdeI
|
4090          4100          4110          4120          4130
* | * * * * *
ATATACAT ATG GCT AGC ATG ACT GGT GGA CAG CAA ATG GGT CGG GAT CCT
M A S M T G G Q Q M G R>
__a__a__a__a__a__a_F10__a__a__a__a__a__a__>
D P>
__b__>

>XhoI
|
4140          4150          4160          4170
* | * * * * *
GAC CTG GAA AAA GAG GCC GAA GAG CTG GAG CAG GAA AAC GCT GAA CTC
D L E K E A E E L E Q E N A E L>
__b__b__TWO AMPHIPATHIC HEPTAD S (3D PHASE- 785) __b__b__>

4180          4190          4200          4210          4220
* | * * * * *
GAG GAA GAG CTG GAA GAC AGC TTT CAC AGT TTG CGG GAC TCA GTC CCA
E E E L E>
__TWO AMPHIPAT__>
D S F H S L R D S V P>
__c__c__c__MAX BHLH DOMAIN__c__c__c__>

4230          4240          4250          4260          4270
* | * * * * *
TCA CTC CAA GGA GAG AAG GCA TCC CGG GCC CAA ATC CTA GAC AAA GCA
S L Q G E K A S R A Q I L D K A>
__c__c__c__c__c__c__MAX BHLH DOMAIN__c__c__c__c__c__c__>

4280          4290          4300          4310          4320
* | * * * * *
ACA GAG TAT ATC CAG TAT ATG CGA AGG AAA AAC CAT ACG CAC CAG CAA
T E Y I Q Y M R R K N H T H Q Q>
__c__c__c__c__c__c__MAX BHLH DOMAIN__c__c__c__c__c__c__>

4330          4340          4350          4360          4370
* | * * * * *
GAC ATT GAT GAC CTC AAG CGG CAG AAT GCT CTT CTG GAG CAA CAA GTC
D I D D L K R Q N A L L E Q Q V>
__c__c__c__c__c__c__MAX BHLH DOMAIN__c__c__c__c__c__c__>

>HindIII
|
4380          4390          4400          4410          4420
* | * * * * *
CGT GCA CTG GAG AAG GCA AGA TCA AGT GCC CAA CTG CAG ACC TGAGGCA
R A L E K A R S S A Q L Q T>
__c__c__c__c__c__c__MAX BHLH DOMAIN__c__c__c__c__c__c__>

AGCTTATC

```



```

BamHI      10              20              30              40
*          *          *          *          *          *          *
GGATCCC AAC GAC AAG AGG CGG ACA CAC AAC GTC TTG GAA CGT CAG AGG
      N  D  K  R  R  T  H  N  V  L  E  R  Q  R>
      ___PUTATIVE;  NCBI GI: 50468; CODON_START=1; C-MYC ___>

50              60              70              80              90
*          *          *          *          *          *          *
AGG AAC GAG CTG AAG CGC AGC TTT TTT GCC CTG CGT GAC CAG ATC CCT
      R  N  E  L  K  R  S  F  F  A  L  R  D  Q  I  P>
      ___PUTATIVE;  NCBI GI: 50468; CODON_START=1; C-MYC PROTEIN; ___>

100             110             120             130             140
*          *          *          *          *          *          *
GAA TTG GAA AAC AAC GAA AAG GCC CCC AAG GTA GTG ATC CTC AAA AAA
      E  L  E  N  N  E  K  A  P  K  V  V  I  L  K  K>
      ___PUTATIVE;  NCBI GI: 50468; CODON_START=1; C-MYC PROTEIN; ___>

150             160             170             180             190
*          *          *          *          *          *          *
GCC ACC GCC TAC ATC CTG TCC ATT CAA GCA GAC GAG CAC AAG CTC ACC
      A  T  A  Y  I  L  S  I  Q  A  D  E  H  K  L  T>
      ___PUTATIVE;  NCBI GI: 50468; CODON_START=1; C-MYC PROTEIN; ___>

200             210             220             230             240
*          *          *          *          *          *          *
TCT GAA AAG GAC TTA TTG AGG AAA CGA CGA GAA CAG TTG AAA CAC AAA
      S  E  K  D  L  L  R  K  R  R  E  Q  L  K  H  K>
      ___PUTATIVE;  NCBI GI: 50468; CODON_START=1; C-MYC PROTEIN; ___>

250             260             270
*          *          *          *          *          *
CTC GAA CAG CTT CGA AAC TCT GGT GCA TAA AAGCTT
      L  E  Q  L  R  N  S  G  A  *>
      ___PUTATIVE;  NCBI GI: 50468; CODON___> Hind III

```

FIG. 29

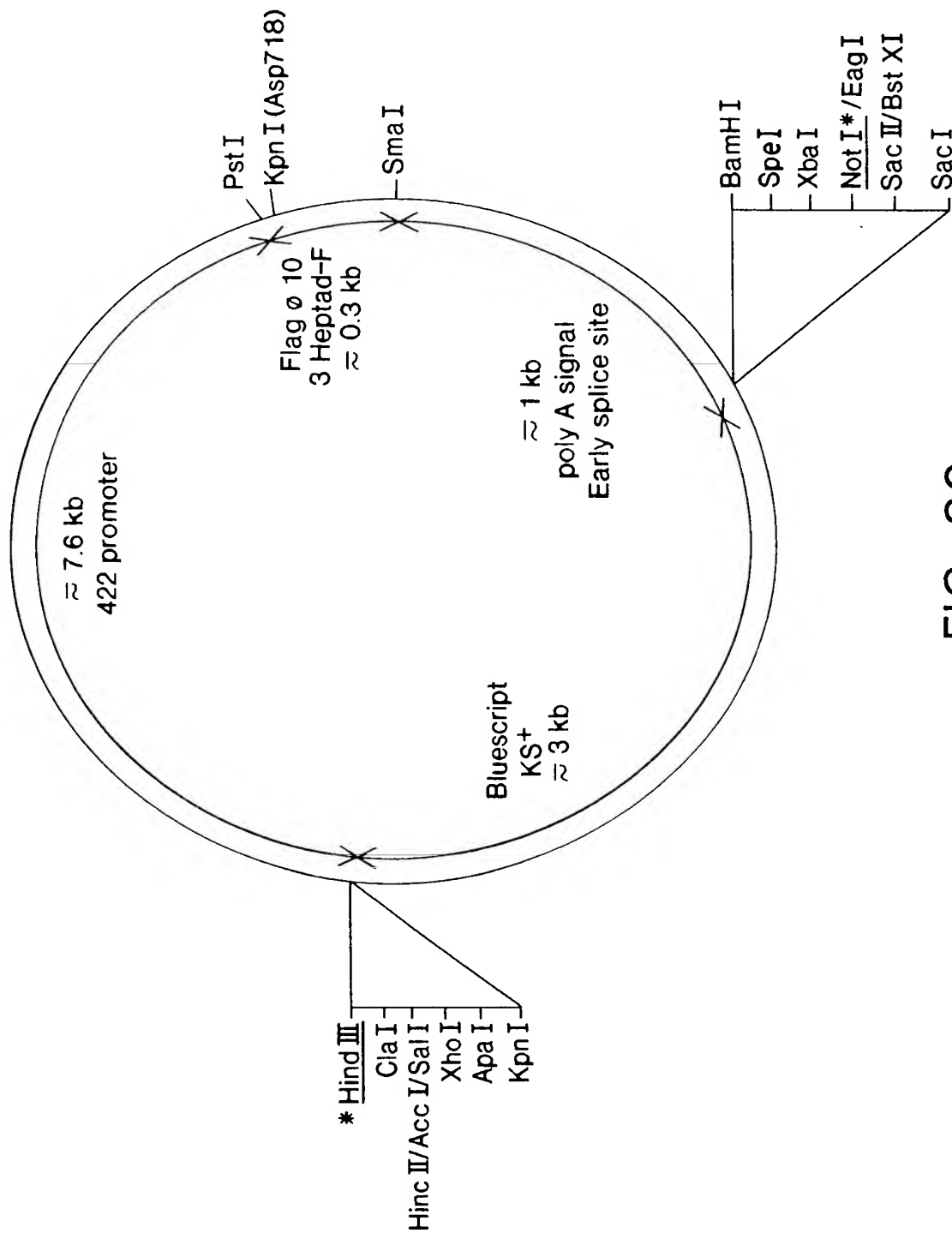


FIG. 30



FIG. 31